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# SEQUENCE LISTING

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 <140> 09/626,813  
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 <150> 60/146,580  
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Asp Gly Met Arg  
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Glu Asp Gly Ile Ser Met Arg Ala Met Asp Pro Ser Arg Val Val Leu
 35             40             45

Ile Asp Leu Asn Leu Pro Ser Ser Ile Phe Ser Lys Tyr Glu Val Val
 50             55             60

Glu Pro Glu Thr Ile Gly Val Asn Met Asp His Leu Lys Lys Ile Leu
 65             70             75             80

Lys Arg Gly Lys Ala Lys Asp Thr Leu Ile Leu Lys Lys Gly Glu Glu
      85             90             95

Asn Phe Leu Glu Ile Thr Ile Gln Gly Thr Ala Thr Arg Thr Phe Arg
 100            105            110

Val Pro Leu Ile Asp Val Glu Glu Met Glu Val Asp Leu Pro Glu Leu
 115            120            125

Pro Phe Thr Ala Lys Val Val Val Leu Gly Glu Val Leu Lys Asp Ala
 130            135            140

Val Lys Asp Ala Ser Leu Val Ser Asp Ser Ile Lys Phe Ile Ala Arg
 145            150            155            160

Glu Asn Glu Phe Ile Met Lys Ala Glu Gly Glu Thr Gln Glu Val Glu
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cgatgaggat atagcgaaga gactaaggta cattgccgaa aatgagggct tagagctaac 2340  
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cattctgcaa gctgcagcag ccttagacaa gaagatcacc gacgaaaacg tattcatggt 2460  
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ggttctgctt gctgataaga taggagagta taacttcaga ctcgttgaag gggctaatga 2700  
aataattcag cttgaagcac tcttagcaca gttcacccta attgggaaga agtgatgaag 2760  
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ccaagaagag gctatagaga aagttagagc gtggatagag agctggttgc atggccaccc 2880  
ccctaagaaa aaagccctat tattagcagg acccccaggg agcggaagaa caaccacagt 2940

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ggaagtcca	aaagagatcc	gagaaaaagc	tgagctagta	gagtacaaga	ggttaaccca	3240
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tctacagacc	gttgtagtgg	gtggttacga	agatgctacg	caagttttgg	catatagaga	3420
tgtagaaaag	acagtctttc	aagccctagg	actcgtcttt	ggaagtgaca	acgccaagag	3480
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tgagaacatt	cctcacctct	acctaaatcc	agaggagatt	gccaggcgt	atgatgcaat	3600
tagtagagcc	gacatatacc	tcggaaggcg	cgccagaact	ggaaactatt	cactctggaa	3660
gtacgcaata	gatatgatga	ctgcaggagt	tgccgtggca	gggagaaaga	gaaggggatt	3720
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anctaactca	cattaattgc	nttgcgctca	ctgccgctt	tccantcggg	aaacctgtcg	4560
tgccagctgc	attaatgaat	cggccaacnc	gcgggganaa	gcggttgcgt	attgggcgct	4620
cttcgcgttc	ctcgcctcatg	actcgcgtcg	ctcggtcntc	ggctgcggcg	aacggtatca	4680
gctcatcaaa	ggcggttaata	cggttatccn	caaatcaggg	gataacgcag	gaaaaaactt	4740
tnnacaaaag	gcnncaaaaag	gcggaaacta	aaaggcgcnt	tctgggtttt	tcntagggccc	4800
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<210> 62

<211> 1603

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid sequence of the genomic RFC clone

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<221> MISC\_FEATURE

<222> (7)

<223> Xaa is any amino acid

<220>

<221> MISC\_FEATURE

<222> (14)

<223> Xaa is any amino acid

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<222> (1269)

<223> Xaa is any amino acid

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<222> (1490)..(1491)

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<222> (1496)

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<222> (1504)

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<222> (1519)

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<222> (1522)

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<222> (1542)

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<222> (1570)

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<222> (1581)

<223> Xaa is any amino acid

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<222> (1586)

<223> Xaa is any amino acid

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<223> Xaa is any amino acid

<400> 62

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Gly Ala Tyr Pro Glu Lys Cys Ser Arg Ser Tyr Ser Gln Leu Ser Ala  
20 25 30

Asp Leu Xaa Phe Phe Leu Leu Phe Phe Cys Ser Val Xaa Ala Asp Lys  
35 40 45

Leu Asn Asn Thr Leu Ile Pro Phe Leu Val Val Cys Glu Ser Met Ser  
50 55 60

Glu Glu Ile Arg Glu Val Lys Val Leu Glu Lys Pro Trp Val Glu Lys  
65 70 75 80

Tyr Arg Pro Gln Arg Leu Asp Asp Ile Val Gly Gln Glu His Ile Val  
85 90 95

Lys Arg Leu Lys His Tyr Val Lys Thr Gly Ser Met Pro His Leu Leu  
100 105 110

Phe Ala Gly Pro Pro Gly Val Gly Lys Cys Leu Thr Gly Asp Thr Lys  
115 120 125

Val Ile Ala Asn Gly Gln Leu Phe Glu Leu Gly Glu Leu Val Glu Lys  
130 135 140

Leu Ser Gly Gly Arg Phe Gly Pro Thr Pro Val Lys Gly Leu Lys Val  
145 150 155 160

Leu Gly Ile Asp Glu Asp Gly Lys Leu Arg Glu Phe Glu Val Gln Tyr  
165 170 175

Val Tyr Lys Asp Arg Thr Asp Arg Leu Ile Lys Ile Lys Thr Gln Leu  
180 185 190

Gly Arg Glu Leu Lys Val Thr Pro Tyr His Pro Leu Leu Val Ile Gly  
195 200 205

Glu Asn Gly Glu Leu Lys Trp Ile Lys Ala Glu Glu Leu Lys Leu Gly  
210 215 220

Asp Lys Leu Ala Ile Pro Ser Phe Leu Pro Leu Ile Thr Gly Glu Asn  
225 230 235 240

Pro Leu Ala Glu Trp Leu Gly Tyr Phe Met Gly Ser Gly Tyr Ala Tyr  
245 250 255

Pro Lys Asn Ser Val Ile Thr Phe Thr Asn Glu Asp Pro Leu Ile Arg

260						265						270					
Gln	Arg	Phe	Met	Glu	Leu	Thr	Glu	Lys	Leu	Phe	Pro	Asp	Ala	Lys	Ile		
275						280						285					
Arg	Glu	Arg	Ile	His	Ala	Asp	Gly	Thr	Pro	Glu	Val	Tyr	Val	Val	Ser		
290						295						300					
Arg	Lys	Ala	Trp	Ser	Leu	Val	Asn	Ser	Ile	Ser	Leu	Thr	Leu	Ile	Pro		
305						310						315					
Arg	Glu	Gly	Trp	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Arg	Ala	Tyr	Ser	Asp		
325						330						335					
Cys	Asn	Gly	Arg	Ile	Glu	Ser	Asp	Ala	Ile	Val	Leu	Ser	Thr	Asp	Asn		
340						345						350					
Asn	Asp	Met	Ala	Gln	Gln	Ile	Ala	Tyr	Ala	Leu	Ala	Ser	Phe	Gly	Ile		
355						360						365					
Ile	Ala	Lys	Met	Asp	Gly	Glu	Asp	Val	Ile	Ile	Ser	Gly	Ser	Asp	Asn		
370						375						380					
Ile	Glu	Arg	Phe	Leu	Asn	Glu	Ile	Gly	Phe	Ser	Thr	Gln	Ser	Lys	Leu		
385						390						395					
Lys	Glu	Ala	Gln	Lys	Leu	Ile	Arg	Lys	Thr	Asn	Val	Arg	Ser	Asp	Gly		
405						410						415					
Leu	Lys	Ile	Asn	Tyr	Glu	Leu	Ile	Ser	Tyr	Val	Lys	Asp	Arg	Leu	Arg		
420						425						430					
Leu	Asn	Val	Asn	Asp	Lys	Arg	Asn	Leu	Ser	Tyr	Arg	Asn	Ala	Lys	Glu		
435						440						445					
Leu	Ser	Trp	Glu	Leu	Met	Lys	Glu	Ile	Tyr	Tyr	Arg	Leu	Glu	Glu	Leu		
450						455						460					
Glu	Arg	Leu	Lys	Lys	Val	Leu	Ser	Glu	Pro	Ile	Leu	Ile	Asp	Trp	Asn		
465						470						475					
Glu	Val	Ala	Lys	Lys	Ser	Asp	Glu	Val	Ile	Glu	Lys	Ala	Lys	Ile	Arg		
485						490						495					
Ala	Glu	Lys	Leu	Leu	Glu	Tyr	Ile	Lys	Gly	Glu	Arg	Lys	Pro	Ser	Phe		
500						505						510					
Lys	Glu	Tyr	Ile	Glu	Ile	Ala	Lys	Val	Leu	Gly	Ile	Asn	Val	Glu	Arg		
515						520						525					
Thr	Ile	Glu	Ala	Met	Lys	Ile	Phe	Ala	Lys	Arg	Tyr	Ser	Ser	Tyr	Ala		
530						535						540					
Glu	Ile	Gly	Arg	Lys	Leu	Gly	Thr	Trp	Asn	Phe	Asn	Val	Lys	Thr	Ile		
545						550						555					
Leu	Glu	Ser	Asp	Thr	Val	Asp	Asn	Val	Glu	Ile	Leu	Glu	Lys	Ile	Arg		
565						570						575					
Lys	Ile	Glu	Leu	Glu	Leu	Ile	Glu	Glu	Ile	Leu	Ser	Asp	Gly	Lys	Leu		
580						585						590					

Lys Glu Gly Ile Ala Tyr Leu Ile Phe Leu Phe Gln Asn Glu Leu Tyr  
 595 600 605  
 Trp Asp Glu Ile Thr Glu Val Lys Glu Leu Arg Gly Asp Phe Ile Ile  
 610 615 620  
 Tyr Asp Leu His Val Pro Gly Tyr His Asn Phe Ile Ala Gly Asn Met  
 625 630 635 640  
 Pro Thr Val Val His Asn Thr Thr Ala Ala Leu Ala Leu Ala Arg Glu  
 645 650 655  
 Leu Phe Gly Glu Asn Trp Arg His Asn Phe Leu Glu Leu Asn Ala Ser  
 660 665 670  
 Asp Glu Arg Gly Ile Asn Val Ile Arg Glu Lys Val Lys Glu Phe Ala  
 675 680 685  
 Arg Thr Lys Pro Ile Gly Gly Ala Ser Phe Lys Ile Ile Phe Leu Asp  
 690 695 700  
 Glu Ala Asp Ala Leu Thr Gln Asp Ala Gln Gln Ala Leu Arg Arg Thr  
 705 710 715 720  
 Met Glu Met Phe Ser Ser Asn Val Arg Phe Ile Leu Ser Cys Asn Tyr  
 725 730 735  
 Ser Ser Lys Ile Ile Glu Pro Ile Gln Ser Arg Cys Ala Ile Phe Arg  
 740 745 750  
 Phe Arg Pro Leu Arg Asp Glu Asp Ile Ala Lys Arg Leu Arg Tyr Ile  
 755 760 765  
 Ala Glu Asn Glu Gly Leu Glu Leu Thr Glu Glu Gly Leu Gln Ala Ile  
 770 775 780  
 Leu Tyr Ile Ala Glu Gly Asp Met Arg Arg Ala Ile Asn Ile Leu Gln  
 785 790 795 800  
 Ala Ala Ala Ala Leu Asp Lys Lys Ile Thr Asp Glu Asn Val Phe Met  
 805 810 815  
 Val Ala Ser Arg Ala Arg Pro Glu Asp Ile Arg Glu Met Met Leu Leu  
 820 825 830  
 Ala Leu Lys Gly Asn Phe Leu Lys Ala Arg Glu Lys Leu Arg Glu Ile  
 835 840 845  
 Leu Leu Lys Gln Gly Leu Ser Gly Glu Asp Val Leu Val Gln Met His  
 850 855 860  
 Lys Glu Val Phe Asn Leu Pro Ile Glu Glu Pro Lys Lys Val Leu Leu  
 865 870 875 880  
 Ala Asp Lys Ile Gly Glu Tyr Asn Phe Arg Leu Val Glu Gly Ala Asn  
 885 890 895  
 Glu Ile Ile Gln Leu Glu Ala Leu Leu Ala Gln Phe Thr Leu Ile Gly  
 900 905 910

Lys Lys Ser Met Pro Glu Leu Pro Trp Val Glu Lys Tyr Arg Pro Lys  
 915 920 925  
 Lys Leu Ser Glu Ile Val Asn Gln Glu Glu Ala Ile Glu Lys Val Arg  
 930 935 940  
 Ala Trp Ile Glu Ser Trp Leu His Gly His Pro Pro Lys Lys Lys Ala  
 945 950 955 960  
 Leu Leu Leu Ala Gly Pro Pro Gly Ser Gly Lys Thr Thr Thr Val Tyr  
 965 970 975  
 Ala Leu Ala Asn Glu Tyr Asn Phe Glu Val Ile Glu Leu Asn Ala Ser  
 980 985 990  
 Asp Glu Arg Thr Tyr Glu Lys Ile Ser Arg Tyr Val Gln Ala Ala Tyr  
 995 1000 1005  
 Thr Met Asp Ile Leu Gly Lys Arg Arg Lys Ile Ile Phe Leu Asp Glu  
 1010 1015 1020  
 Ala Asp Asn Ile Glu Pro Ser Gly Ala Lys Glu Ile Ala Lys Leu Ile  
 1025 1030 1035 1040  
 Asp Lys Ala Lys Asn Pro Ile Ile Met Ala Ala Asn Lys Tyr Trp Glu  
 1045 1050 1055  
 Val Pro Lys Glu Ile Arg Glu Lys Ala Glu Leu Val Glu Tyr Lys Arg  
 1060 1065 1070  
 Leu Thr Gln Arg Asp Val Met Asn Ala Leu Ile Arg Ile Leu Lys Arg  
 1075 1080 1085  
 Glu Gly Ile Thr Val Pro Lys Glu Ile Leu Leu Glu Ile Ala Lys Arg  
 1090 1095 1100  
 Ser Ser Gly Asp Leu Arg Ala Ala Ile Asn Asp Leu Gln Thr Val Val  
 1105 1110 1115 1120  
 Val Gly Gly Tyr Glu Asp Ala Thr Gln Val Leu Ala Tyr Arg Asp Val  
 1125 1130 1135  
 Glu Lys Thr Val Phe Gln Ala Leu Gly Leu Val Phe Gly Ser Asp Asn  
 1140 1145 1150  
 Ala Lys Arg Ala Lys Met Ala Met Trp Asn Leu Asp Met Ser Pro Asp  
 1155 1160 1165  
 Glu Phe Leu Leu Trp Val Asp Glu Asn Ile Pro His Leu Tyr Leu Asn  
 1170 1175 1180  
 Pro Glu Glu Ile Ala Gln Ala Tyr Asp Ala Ile Ser Arg Ala Asp Ile  
 1185 1190 1195 1200  
 Tyr Leu Gly Arg Ala Ala Arg Thr Gly Asn Tyr Ser Leu Trp Lys Tyr  
 1205 1210 1215  
 Ala Ile Asp Met Met Thr Ala Gly Val Ala Val Ala Gly Arg Lys Arg  
 1220 1225 1230  
 Arg Gly Phe Val Lys Phe Tyr Pro Pro Asn Thr Leu Lys Ile Leu Ala



1235	1240	1245
Glu Ser Lys Glu Glu Arg Glu Ile Arg Glu Ser Ile Ile Lys Lys Ile 1250 1255 1260		
Ile Arg Glu Met Xaa Met Ser Arg Leu Gln Ala Ile Glu Thr Met Lys 1265 1270 1275 1280		
Ile Ile Arg Glu Ile Phe Glu Asn Asn Leu Asp Leu Ala Ala His Phe 1285 1290 1295		
Thr Val Phe Leu Gly Leu Ser Glu Lys Glu Val Glu Phe Leu Ala Gly 1300 1305 1310		
Lys Glu Lys Ala Gly Thr Ile Trp Gly Lys Ala Leu Ala Leu Arg Arg 1315 1320 1325		
Lys Leu Lys Glu Leu Gly Ile Arg Glu Glu Glu Lys Pro Lys Val Glu 1330 1335 1340		
Ile Glu Glu Glu Glu Glu Glu Glu Lys Thr Glu Glu Glu Lys Glu 1345 1350 1355 1360		
Glu Ile Glu Glu Lys Pro Glu Glu Glu Lys Glu Glu Glu Lys Lys Glu 1365 1370 1375		
Lys Glu Lys Pro Lys Lys Gly Lys Gln Ala Thr Leu Phe Asp Phe Leu 1380 1385 1390		
Lys Lys Leu Pro Phe Phe Phe Tyr Ser Ser Glu Ser Trp Pro Ser Asn 1395 1400 1405		
Phe Phe Tyr Cys Leu Leu His Ile Asn Leu Tyr Glu Leu Glu Phe Leu 1410 1415 1420		
Gln Pro Gly Gly Ser Thr Ser Ser Arg Ala Ala Ala Thr Ala Val Glu 1425 1430 1435 1440		
Leu Gln Leu Leu Phe Pro Leu Val Arg Val Asn Phe Glu Leu Gly Val 1445 1450 1455		
Ile Met Val Ile Ala Val Ser Cys Val Lys Leu Leu Ser Ala His Asn 1460 1465 1470		
Ser Thr Gln His Thr Asn Pro Glu Ala Ile Val Asn Pro Gly Val Pro 1475 1480 1485		
Asn Xaa Xaa Asn Ser His Leu Xaa Cys Ala His Cys Pro Leu Ser Xaa 1490 1495 1500		
Arg Glu Thr Cys Arg Ala Ser Cys Ile Asn Glu Ser Ala Asn Xaa Arg 1505 1510 1515 1520		
Gly Xaa Ala Val Ala Tyr Trp Ala Leu Phe Arg Phe Leu Ala His Asp 1525 1530 1535		
Ser Leu Arg Ser Val Xaa Gly Cys Gly Glu Arg Tyr Gln Leu Ile Lys 1540 1545 1550		
Gly Gly Asn Thr Val Ile Xaa Lys Ser Gly Asp Asn Ala Gly Lys Asn 1555 1560 1565		

Phe Xaa Gln Lys Ala Xaa Lys Gly Gly Asn Lys Ala Xaa Ser Gly Phe  
1570 1575 1580

Phe Xaa Gly Pro Pro Arg Xaa Leu Xaa Lys Ser Thr His Ser Ser Gly  
1585 1590 1595 1600

Lys Pro Lys

<210> 63

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
P55 clone

<220>

<221> MISC FEATURE

<222> (354)

<223> Xaa is any amino acid

<400> 63

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Glu Ile Val Asn Gln Glu Glu Ala Ile Glu Lys Val Arg Ala Trp Ile  
20 25 30

Glu Ser Trp Leu His Gly His Pro Pro Lys Lys Lys Ala Leu Leu Leu  
35 40 45

Ala Gly Pro Pro Gly Ser Gly Lys Thr Thr Thr Val Tyr Ala Leu Ala  
50 55 60

Asn Glu Tyr Asn Phe Glu Val Ile Glu Leu Asn Ala Ser Asp Glu Arg  
65 70 75 80

Thr Tyr Glu Lys Ile Ser Arg Tyr Val Gln Ala Ala Tyr Thr Met Asp  
85 90 95

Ile Leu Gly Lys Arg Arg Lys Ile Ile Phe Leu Asp Glu Ala Asp Asn  
100 105 110

Ile Glu Pro Ser Gly Ala Lys Glu Ile Ala Lys Leu Ile Asp Lys Ala  
115 120 125

Lys Asn Pro Ile Ile Met Ala Ala Asn Lys Tyr Trp Glu Val Pro Lys  
130 135 140

Glu Ile Arg Glu Lys Ala Glu Leu Val Glu Tyr Lys Arg Leu Thr Gln  
145 150 155 160

Arg Asp Val Met Asn Ala Leu Ile Arg Ile Leu Lys Arg Glu Gly Ile  
165 170 175

Thr Val Pro Lys Glu Ile Leu Leu Glu Ile Ala Lys Arg Ser Ser Gly  
180 185 190

Asp	Leu	Arg	Ala	Ala	Ile	Asn	Asp	Leu	Gln	Thr	Val	Val	Val	Gly	Gly	195	200	205	
Tyr	Glu	Asp	Ala	Thr	Gln	Val	Leu	Ala	Tyr	Arg	Asp	Val	Glu	Lys	Thr	210	215	220	
Val	Phe	Gln	Ala	Leu	Gly	Leu	Val	Phe	Gly	Ser	Asp	Asn	Ala	Lys	Arg	225	230	235	240
Ala	Lys	Met	Ala	Met	Trp	Asn	Leu	Asp	Met	Ser	Pro	Asp	Glu	Phe	Leu	245	250	255	
Leu	Trp	Val	Asp	Glu	Asn	Ile	Pro	His	Leu	Tyr	Leu	Asn	Pro	Glu	Glu	260	265	270	
Ile	Ala	Gln	Ala	Tyr	Asp	Ala	Ile	Ser	Arg	Ala	Asp	Ile	Tyr	Leu	Gly	275	280	285	
Arg	Ala	Ala	Arg	Thr	Gly	Asn	Tyr	Ser	Leu	Trp	Lys	Tyr	Ala	Ile	Asp	290	295	300	
Met	Met	Thr	Ala	Gly	Val	Ala	Val	Val	Gly	Arg	Lys	Arg	Arg	Gly	Phe	305	310	315	320
Val	Lys	Phe	Tyr	Pro	Pro	Asn	Thr	Leu	Lys	Ile	Leu	Ala	Glu	Ser	Lys	325	330	335	
Glu	Glu	Arg	Glu	Ile	Arg	Glu	Ser	Ile	Ile	Lys	Lys	Ile	Ile	Arg	Glu	340	345	350	
Met	Xaa	Met	Ser	Arg	Leu	Gln	Ala	Ile	Glu	Thr	Met	Lys	Ile	Ile	Arg	355	360	365	
Glu	Ile	Phe	Glu	Asn	Asn	Leu	Asp	Leu	Ala	Ala	His	Phe	Thr	Val	Phe	370	375	380	
Leu	Gly	Leu	Ser	Glu	Lys	Glu	Val	Glu	Phe	Leu	Ala	Gly	Lys	Glu	Lys	385	390	395	400
Ala	Gly	Thr	Ile	Trp	Gly	Lys	Ala	Leu	Ala	Leu	Arg	Arg	Lys	Leu	Lys	405	410	415	
Glu	Leu	Gly	Ile	Arg	Glu	Glu	Glu	Lys	Pro	Lys	Val	Glu	Ile	Glu	Glu	420	425	430	
Glu	Glu	Glu	Glu	Glu	Glu	Lys	Thr	Glu	Glu	Glu	Lys	Glu	Glu	Ile	Glu	435	440	445	
Glu	Lys	Pro	Glu	Glu	Glu	Lys	Glu	Glu	Glu	Lys	Lys	Glu	Lys	Glu	Lys	450	455	460	
Pro	Lys	Lys	Gly	Lys	Gln	Ala	Thr	Leu	Phe	Asp	Phe	Leu	Lys	Lys		465	470	475	

<210> 64

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
P38 clone

<400> 64

Met	Ser	Glu	Glu	Ile	Arg	Glu	Val	Lys	Val	Leu	Glu	Lys	Pro	Trp	Val	1	5	10	15
Glu	Lys	Tyr	Arg	Pro	Gln	Arg	Leu	Asp	Asp	Ile	Val	Gly	Gln	Glu	His	20	25	30	
Ile	Val	Lys	Arg	Leu	Lys	His	Tyr	Val	Lys	Thr	Gly	Ser	Met	Pro	His	35	40	45	
Leu	Leu	Phe	Ala	Gly	Pro	Pro	Gly	Val	Gly	Lys	Thr	Thr	Ala	Ala	Leu	50	55	60	
Ala	Leu	Ala	Arg	Glu	Leu	Phe	Gly	Glu	Asn	Trp	Arg	His	Asn	Phe	Leu	65	70	75	80
Glu	Leu	Asn	Ala	Ser	Asp	Glu	Arg	Gly	Ile	Asn	Val	Ile	Arg	Glu	Lys	85	90	95	
Val	Lys	Glu	Phe	Ala	Arg	Thr	Lys	Pro	Ile	Gly	Gly	Ala	Ser	Phe	Lys	100	105	110	
Ile	Ile	Phe	Leu	Asp	Glu	Ala	Asp	Ala	Leu	Thr	Gln	Asp	Ala	Gln	Gln	115	120	125	
Ala	Leu	Arg	Arg	Thr	Met	Glu	Met	Phe	Ser	Ser	Asn	Val	Arg	Phe	Ile	130	135	140	
Leu	Ser	Cys	Asn	Tyr	Ser	Ser	Lys	Ile	Ile	Glu	Pro	Ile	Gln	Ser	Arg	145	150	155	160
Cys	Ala	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Arg	Asp	Glu	Asp	Ile	Ala	Lys	165	170	175	
Arg	Leu	Arg	Tyr	Ile	Ala	Glu	Asn	Glu	Gly	Leu	Glu	Leu	Thr	Glu	Glu	180	185	190	
Gly	Leu	Gln	Ala	Ile	Leu	Tyr	Ile	Ala	Glu	Gly	Asp	Met	Arg	Arg	Ala	195	200	205	
Ile	Asn	Ile	Leu	Gln	Ala	Ala	Ala	Ala	Leu	Asp	Lys	Lys	Ile	Thr	Asp	210	215	220	
Glu	Asn	Val	Phe	Met	Val	Ala	Ser	Arg	Ala	Arg	Pro	Glu	Asp	Ile	Arg	225	230	235	240
Glu	Met	Met	Leu	Leu	Ala	Leu	Lys	Gly	Asn	Phe	Leu	Lys	Ala	Arg	Glu	245	250	255	
Lys	Leu	Arg	Glu	Ile	Leu	Leu	Lys	Gln	Gly	Leu	Ser	Gly	Glu	Asp	Val	260	265	270	
Leu	Val	Gln	Met	His	Lys	Glu	Val	Phe	Asn	Leu	Pro	Ile	Glu	Glu	Pro	275	280	285	
Lys	Lys	Val	Leu	Leu	Ala	Asp	Lys	Ile	Gly	Glu	Tyr	Asn	Phe	Arg	Leu	290	295	300	

Val Glu Gly Ala Asn Glu Ile Ile Gln Leu Glu Ala Leu Leu Ala Gln  
 305 310 315 320

Phe Thr Leu Ile Gly Lys Lys  
 325

<210> 65  
 <211> 1077  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: RFA clone

<400> 65  
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 catgcagctg ctctcttact agcagaaaagg ctgggagttg aagttaccaa aagagaagaa 180  
 caacctttaa tgaagattag cgacctatat ccaggaatgg atccccacga ggtcaacatt 240  
 gttggaagaa tacttaagaa gtatccaccg cgagaataca caaagaagga tggaagcatt 300  
 ggaaggggtt ccagtctagt tatatacgat gatactggga gagcgagggt tgttcttttg 360  
 gattcaaaag ttttggagta ttacagcaag ctagaagtag gggatgttat taaggtttta 420  
 gacgcccagg ttagggagag cttatctggt ttgcctgaat tgcacattaa cttcagggct 480  
 agaataatta aaaaccacga tgatcctagg gtccaggata tcccacctct tgaagaagtt 540  
 agagtggcaa cttatacgag aaagaagatc agtgagggtc agcctgggga tagatttgta 600  
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 tgtaagaaga aggttgacta tgaccagga atggacgttt ggatagtcc agaacatgga 720  
 gaggttgagc caataaaaat cactattctt gactttgggc ttgatgatgg ctcgggatac 780  
 attaggatta ccctcttttg agacgatgct gaagagttgc tgggagtagg gccagaagag 840  
 attgcccaga agcttaagga aatggagagc atgggcatga ctctcaagga ggcagcgaga 900  
 aaattggcgg aggaagagtt ctacaatata atagggaag aaataatcgt gaggggaaat 960  
 gtaattgagg acaggttctt gggcctaatac ttaagggcct cctcctggga agaagttgac 1020  
 tacaagagag aaattgagag aattaagagg gaattggaag aattgggggt gatgtga 1077

<210> 66  
 <211> 360  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Amino acid  
 sequence of RFA clone

<400> 66  
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 1 5 10 15  
 Glu Glu Val Glu Gly Ile Thr Leu Glu Glu Ile Glu Asn Gln Ile Arg  
 20 25 30  
 Gln Ile Met Arg Glu Asn Asn Ile Ser Glu His Ala Ala Ala Leu Leu  
 35 40 45  
 Leu Ala Glu Arg Leu Gly Val Glu Val Thr Lys Arg Glu Glu Gln Pro  
 50 55 60  
 Leu Met Lys Ile Ser Asp Leu Tyr Pro Gly Met Asp Pro His Glu Val  
 65 70 75 80

Asn	Ile	Val	Gly	Arg	Ile	Leu	Lys	Lys	Tyr	Pro	Pro	Arg	Glu	Tyr	Thr	85	90	95
Lys	Lys	Asp	Gly	Ser	Ile	Gly	Arg	Val	Ala	Ser	Leu	Val	Ile	Tyr	Asp	100	105	110
Asp	Thr	Gly	Arg	Ala	Arg	Val	Val	Leu	Trp	Asp	Ser	Lys	Val	Leu	Glu	115	120	125
Tyr	Tyr	Ser	Lys	Leu	Glu	Val	Gly	Asp	Val	Ile	Lys	Val	Leu	Asp	Ala	130	135	140
Gln	Val	Arg	Glu	Ser	Leu	Ser	Gly	Leu	Pro	Glu	Leu	His	Ile	Asn	Phe	145	150	155
Arg	Ala	Arg	Ile	Ile	Lys	Asn	Pro	Asp	Asp	Pro	Arg	Val	Gln	Asp	Ile	165	170	175
Pro	Pro	Leu	Glu	Glu	Val	Arg	Val	Ala	Thr	Tyr	Thr	Arg	Lys	Lys	Ile	180	185	190
Ser	Glu	Val	Glu	Pro	Gly	Asp	Arg	Phe	Val	Glu	Leu	Arg	Gly	Thr	Ile	195	200	205
Ala	Lys	Val	Tyr	Arg	Val	Leu	Val	Tyr	Asp	Ala	Cys	Pro	Glu	Cys	Lys	210	215	220
Lys	Lys	Val	Asp	Tyr	Asp	Pro	Gly	Met	Asp	Val	Trp	Ile	Cys	Pro	Glu	225	230	235
His	Gly	Glu	Val	Glu	Pro	Ile	Lys	Ile	Thr	Ile	Leu	Asp	Phe	Gly	Leu	245	250	255
Asp	Asp	Gly	Ser	Gly	Tyr	Ile	Arg	Ile	Thr	Leu	Phe	Gly	Asp	Asp	Ala	260	265	270
Glu	Glu	Leu	Leu	Gly	Val	Gly	Pro	Glu	Glu	Ile	Ala	Gln	Lys	Leu	Lys	275	280	285
Glu	Met	Glu	Ser	Met	Gly	Met	Thr	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	290	295	300
Ala	Glu	Glu	Glu	Phe	Tyr	Asn	Ile	Ile	Gly	Lys	Glu	Ile	Ile	Val	Arg	305	310	315
Gly	Asn	Val	Ile	Glu	Asp	Arg	Phe	Leu	Gly	Leu	Ile	Leu	Arg	Ala	Ser	325	330	335
Ser	Trp	Glu	Glu	Val	Asp	Tyr	Lys	Arg	Glu	Ile	Glu	Arg	Ile	Lys	Arg	340	345	350
Glu	Leu	Glu	Glu	Leu	Gly	Val	Met									355	360	

<210> 67

<211> 2604

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 2

<400> 67

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aagaggctcg gatttagact ttattctcac caagttaaag ccctagaaaa gctgtattca 180
gggaaaaacg tagttgtttc aacgcccaca gctagtggga aaagcgagat atttaggttg 240
tttatctttg acgaaatact gtcaagcccg tcctcaactt ttctcttaat ctaccaaca 300
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atgtgtggaa aaagagttcg agcagaagtc ttaactggag atacggaatg ggaaaagaga 420
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aaggaagctg gaagtccaag cccgagaaga attatagta tgtttgagcc aagaaggttt 780
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2604

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<210> 68

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 3

<400> 68

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gcaattgaaa	gaatagcccc	agtgttcaat	aagagaagag	tggtagaaga	cacaatcagg	2460
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<210> 69

<211> 2943

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 4

<400> 69

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<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 5

<400> 70

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<210> 71

<211> 2823

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 6

<400> 71

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ataatatcaa	tagacctagc	taagagatac	accgaggaaa	tactccgtca	aaagtgggat	420
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cgaactaaga	aggttgtcaa	cgaacttgaa	ggagaagtgt	tcaagaagtg	tcactttggg	720
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<210> 72

<211> 3837

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 7

<400> 72

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<210> 73

<211> 1968

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase dna2

<400> 73

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<210> 74

<211> 867

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 2

<400> 74

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Asn Glu Glu Val Asn Glu Leu Val Lys Arg Leu Gly Phe Arg Leu Tyr
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Ser His Gln Val Lys Ala Leu Glu Lys Leu Tyr Ser Gly Lys Asn Val
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Val Val Ser Thr Pro Thr Ala Ser Gly Lys Ser Glu Ile Phe Arg Leu
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Phe Ile Phe Asp Glu Ile Leu Ser Ser Pro Ser Ser Thr Phe Leu Leu
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Ile Tyr Pro Thr Arg Ala Leu Ile Asn Asn Gln Met Glu Lys Phe Glu
 100          105          110

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 115 120 125  
 Glu Val Leu Thr Gly Asp Thr Glu Trp Glu Lys Arg Arg Glu Ile Ile  
 130 135 140  
 Arg Ser Lys Pro Asn Val Ile Phe Thr Thr Pro Asp Met Leu His His  
 145 150 155 160  
 His Ile Leu Pro Arg Trp Arg Asp Tyr Phe Trp Leu Leu Lys Gly Leu  
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 Arg Leu Leu Val Val Asp Glu Leu His Val Tyr Arg Gly Ile Phe Gly  
 180 185 190  
 Thr Asn Val Ala Tyr Val Phe Lys Arg Leu Phe Leu Arg Leu Lys Arg  
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 Leu Ser Ser Ser Pro Gln Ile Leu Ala Leu Ser Ala Thr Leu Arg Asn  
 210 215 220  
 Pro Lys Glu Phe Ala Glu Gln Phe Phe Glu Thr Glu Phe Glu Glu Val  
 225 230 235 240  
 Lys Glu Ala Gly Ser Pro Ser Pro Arg Arg Ile Ile Val Met Phe Glu  
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 Pro Arg Arg Phe Thr Gly Glu Gln Leu Ile Lys Gln Ile Val Glu Arg  
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 Gly Thr Glu Arg Ile Met Arg Leu Phe Leu Phe Ser Asp Ala Phe Asp  
 290 295 300  
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 305 310 315 320  
 Ile Glu Arg Asp Phe Arg Glu Gly Asn Leu Thr Val Leu Leu Thr Thr  
 325 330 335  
 Asn Ala Leu Glu Leu Gly Ile Asp Ile Gly Asp Leu Asp Ala Val Ile  
 340 345 350  
 Asn Tyr Gly Ile Pro Ser Asp Gly Leu Phe Ser Leu Ile Gln Arg Phe  
 355 360 365  
 Gly Arg Ala Gly Arg Asp Pro Asn Arg Ile Ala Ile Asn Gly Ile Ile  
 370 375 380  
 Leu Arg Arg Asn Gly Leu Asp Tyr Tyr Tyr Lys Glu His Phe Asp Glu  
 385 390 395 400  
 Leu Val Glu Gly Ile Glu Lys Gly Leu Val Glu Lys Ile Pro Val Asn  
 405 410 415  
 Leu Asp Asn Glu Lys Ile Ala Lys Lys His Leu His Tyr Ala Ile Ala  
 420 425 430

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Phe	Ile	Lys	Thr	Leu	Val	Glu	Glu	Gly	Tyr	Val	Glu	Val	Thr	Arg	Asn		
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Ser	Ser	Ile	Arg	Thr	Ala	Ser	Asp	Glu	Ser	Tyr	Phe	Leu	Val	Val	Asp		
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545					550					555					560		
Lys	Phe	His	Phe	Val	Phe	Ala	Arg	Pro	Leu	Pro	Ile	Glu	Glu	Glu	Ile		
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Phe	Trp	Leu	Glu	Phe	Pro	Asn	Asp	Ile	Arg	Ile	Val	Pro	Glu	Glu	Glu		
		675					680					685					
Phe	Arg	Glu	Phe	Phe	Ala	Val	Ala	Ser	Glu	Ile	Asp	Pro	Glu	Leu	Ala		
	690					695					700						
Met	Phe	Leu	Tyr	Asn	Arg	Ile	Ser	Arg	Lys	Ser	Leu	Phe	Pro	Thr	Leu		
705					710					715					720		
Leu	Gly	Ala	Thr	Thr	His	Tyr	Ile	Arg	Ser	Phe	Ile	Leu	His	His	Ala		
				725					730					735			
Lys	Asp	Lys	Gly	Glu	Glu	Phe	Ala	Phe	Ala	Val	Lys	Lys	Met	Ile	Asp		
			740					745					750				
Ser	Lys	Asp	Gly	Ile	Gly	Ser	Gly	Leu	His	Ala	Ile	Glu	Pro	Asn	Ile		

755

760

765

Ile Lys Leu Ala Pro Val Val Thr His Val Asp Ser Arg Glu Ile Gly  
 770 775 780

Gly Tyr Ser Tyr Asp Asp Phe His Gly Lys Pro Val Ile Phe Ile Tyr  
 785 790 795 800

Asp Gly Asn Glu Gly Gly Ser Gly Ile Ile Arg Gln Val Tyr Glu Asn  
 805 810 815

Val Glu Lys Leu Met Tyr Arg Ser Leu Glu His Ile Lys Lys Cys Pro  
 820 825 830

Cys Lys Asp Gly Cys Pro Ala Cys Ile Tyr Ser Pro Lys Cys Gly Thr  
 835 840 845

Phe Asn Glu Phe Leu Asp Lys Trp Met Ala Ile Arg Ile Trp Glu Lys  
 850 855 860

Val Leu Pro  
 865

<210> 75

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 3

<400> 75

Met Leu Ile Val Val Arg Pro Gly Arg Lys Lys Asn Glu Leu Glu Ala  
 1 5 10 15

Phe Ile Ile Glu Asn Pro Pro Glu Lys Leu Ser Gln Arg Arg Asn Leu  
 20 25 30

Lys Ala Asp Arg Val Val Arg Leu Ile Met Arg Asp Asn Arg Leu Phe  
 35 40 45

Lys Ala Leu Glu Gly Ser Gln Tyr Leu Asn Pro Lys Glu Val Glu Arg  
 50 55 60

Ala Leu Arg Asn Ser Arg Ile Val Leu Val Asn Ala Asn Glu Trp Glu  
 65 70 75 80

Glu Tyr Phe Lys Lys Arg Leu Met Asn Lys Arg Val Glu Lys Ala Asp  
 85 90 95

Ile Cys Arg Leu Cys Leu Leu Asn Gly Lys Ile Thr Val Leu Thr Glu  
 100 105 110

Gly Asn Arg Ile Arg Tyr Arg Asp Glu Tyr Ile Cys Glu Ser Cys Ala  
 115 120 125

Glu Glu Glu Leu Lys Arg Glu Leu Arg Phe Arg Phe Asn Ser Ile Gly  
 130 135 140

Met Leu Glu Gln Ala Lys Lys Leu Leu Glu Arg Phe Arg Asp Leu Asp



145		150		155		160
Lys Val Ile Ser	Ile Phe Asp Pro Ser Phe Asp Pro Thr Lys His Pro	165		170		175
Glu Ile Thr Lys	Trp Asp Glu Leu Lys Ala Lys His Ile Arg Val Glu	180		185		190
Lys Met His Ile	Asp Glu Leu Asn Ile Pro Glu Glu Phe Lys Lys Val	195		200		205
Leu Lys Ala Glu	Gly Ile Asn Glu Leu Leu Pro Val Gln Val Leu Ala	210		215		220
Ile Lys Asn Gly	Leu Leu Glu Gly Glu Asn Leu Leu Val Val Ser Ala	225		230		235
Thr Ala Ser Gly	Lys Thr Leu Ile Gly Glu Leu Ala Gly Ile Pro Lys	245		250		255
Ala Leu Lys Gly	Lys Lys Met Leu Phe Leu Val Pro Leu Val Ala Leu	260		265		270
Ala Asn Gln Lys	Tyr Glu Asp Phe Lys Arg Arg Tyr Ser Lys Leu Gly	275		280		285
Leu Lys Val Ala	Ile Arg Val Gly Met Ser Arg Ile Lys Thr Lys Glu	290		295		300
Glu Pro Ile Val	Leu Asp Thr Gly Thr Asp Ala His Ile Ile Val Gly	305		310		315
Thr Tyr Glu Gly	Ile Asp Tyr Leu Leu Arg Ala Gly Lys Lys Ile Gly	325		330		335
Asn Val Gly Thr	Val Val Ile Asp Glu Ile His Met Leu Asp Asp Glu	340		345		350
Glu Arg Gly Ala	Arg Leu Asp Gly Leu Ile Ala Arg Leu Arg Lys Leu	355		360		365
Tyr Ser Asn Ala	Gln Phe Ile Gly Leu Ser Ala Thr Val Gly Asn Pro	370		375		380
Gln Glu Leu Ala	Arg Lys Leu Gly Met Lys Leu Val Leu Tyr Asp Glu	385		390		395
Arg Pro Val Asp	Leu Glu Arg His Leu Ile Ile Ala Arg Asn Glu Ser	405		410		415
Glu Lys Trp Arg	Tyr Ile Ala Lys Leu Cys Lys Ala Glu Ala Met Arg	420		425		430
Lys Ser Glu Lys	Gly Phe Lys Gly Gln Thr Ile Val Phe Thr Phe Ser	435		440		445
Arg Arg Arg Cys	His Glu Leu Ala Ser Phe Leu Thr Gly Gln Gly Leu	450		455		460
Lys Ala Lys Ala	Tyr His Ser Gly Leu Pro Tyr Val Gln Arg Lys Leu	465		470		475
						480

Thr	Glu	Met	Glu	Phe	Gln	Ala	Gln	Met	Ile	Asp	Val	Val	Val	Thr	Thr	485	490	495
Ala	Ala	Leu	Gly	Ala	Gly	Val	Asp	Phe	Pro	Ala	Ser	Gln	Val	Ile	Phe	500	505	510
Glu	Ser	Leu	Ala	Met	Gly	Asn	Lys	Trp	Ile	Thr	Val	Arg	Glu	Phe	His	515	520	525
Gln	Met	Leu	Gly	Arg	Ala	Gly	Arg	Pro	Gln	Tyr	His	Glu	Lys	Gly	Lys	530	535	540
Val	Tyr	Ile	Ile	Val	Glu	Pro	Gly	Lys	Lys	Tyr	Ser	Ala	Gln	Met	Glu	545	550	555
Gly	Thr	Glu	Asp	Glu	Val	Ala	Leu	Lys	Leu	Leu	Thr	Ser	Pro	Ile	Glu	565	570	575
Pro	Val	Ile	Val	Glu	Trp	Ser	Asp	Glu	Phe	Glu	Glu	Asp	Asn	Val	Leu	580	585	590
Ala	His	Ala	Cys	Val	Phe	Asn	Arg	Leu	Lys	Val	Ile	Glu	Glu	Val	Gln	595	600	605
Ser	Leu	Cys	Leu	Gly	Ala	Asn	Gln	Ser	Ala	Lys	Asn	Val	Leu	Glu	Lys	610	615	620
Leu	Met	Glu	Lys	Gly	Leu	Val	Lys	Ile	Tyr	Gly	Asp	Lys	Val	Glu	Ala	625	630	635
Thr	Pro	Tyr	Gly	Arg	Ala	Val	Ser	Met	Ser	Phe	Leu	Leu	Pro	Arg	Glu	645	650	655
Ala	Glu	Phe	Ile	Arg	Asp	Asn	Leu	Glu	Ser	Thr	Asp	Pro	Ile	Glu	Ile	660	665	670
Ala	Ile	Lys	Leu	Leu	Pro	Phe	Glu	Asn	Val	Tyr	Leu	Pro	Gly	Ser	Leu	675	680	685
Gln	Arg	Glu	Ile	Glu	Ser	Ala	Val	Arg	Gly	Lys	Ile	Ser	Ser	Asn	Ile	690	695	700
Phe	Ser	Ser	Ser	Phe	Ala	Ser	Val	Leu	Glu	Glu	Leu	Asp	Lys	Ile	Ile	705	710	715
Pro	Glu	Ile	Ser	Pro	Asn	Ala	Ala	Glu	Arg	Leu	Phe	Leu	Ile	Tyr	Gln	725	730	735
Asp	Phe	Phe	Asn	Cys	Pro	Glu	Gln	Asp	Cys	Thr	Glu	Phe	Ala	Met	Glu	740	745	750
Arg	Ile	Gly	Arg	Lys	Ile	Ile	Asp	Leu	Arg	Arg	Glu	Gly	Tyr	Glu	Pro	755	760	765
Ser	Lys	Ile	Ser	Glu	His	Phe	Arg	Lys	Val	Tyr	Ala	Leu	Ile	Leu	Tyr	770	775	780
Pro	Gly	Asp	Val	Phe	Thr	Trp	Leu	Asp	Gly	Ile	Val	Arg	Lys	Leu	Glu	785	790	795
																		800

Ala Ile Glu Arg Ile Ala Arg Val Phe Asn Lys Arg Arg Val Val Glu  
805 810 815

Asp Thr Ile Arg Val Arg Arg Glu Ile Glu Glu Gly Lys Ile Leu Lys  
820 825 830

Gly Glu Arg Arg  
835

<210> 76

<211> 980

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 4

<400> 76

Met His Lys Tyr Phe Phe Pro Leu Pro Ala Thr Lys Ser Thr Phe Leu  
1 5 10 15

Leu Pro Ala Asp Leu Thr Thr Ala Asn Pro Cys Phe Ser Lys Ser Leu  
20 25 30

Ile Asn Ser Leu Ser Ala Trp Ala Pro Phe Leu Tyr Ile Gln Cys Phe  
35 40 45

Ser Tyr Leu Pro Leu Ile Asn Phe Leu Asn Ser Leu Thr Tyr Pro Leu  
50 55 60

Glu Met His Ile Leu Ile Lys Lys Ala Ile Lys Glu Arg Phe Gly Lys  
65 70 75 80

Leu Asn Ala Leu Gln Gln Leu Ala Phe His Lys Ile Arg Gly Glu Gly  
85 90 95

Lys Ser Val Leu Ile Ile Ala Pro Thr Gly Ser Gly Lys Thr Glu Ala  
100 105 110

Ala Val Ile Pro Ile Leu Asp Ala Ile Leu Arg Glu Asn Leu Lys Pro  
115 120 125

Ile Ala Ala Ile Tyr Ile Ala Pro Leu Lys Ala Leu Asn Arg Asp Leu  
130 135 140

Leu Glu Arg Leu Lys Trp Trp Glu Glu Lys Thr Gly Val Ile Ile Glu  
145 150 155 160

Val Arg His Gly Asp Thr Pro Thr Ser Lys Arg Leu Lys Gln Val Lys  
165 170 175

Asn Pro Pro His Leu Leu Ile Thr Thr Pro Glu Met Leu Pro Ala Ile  
180 185 190

Leu Thr Thr Lys Ser Phe Arg Pro Tyr Leu Lys Asn Thr Lys Phe Ile  
195 200 205

Val Ile Asp Glu Ile Gly Glu Leu Ile Glu Asn Lys Arg Gly Thr Gln  
210 215 220

Leu	Ile	Leu	Asn	Leu	Lys	Arg	Leu	Glu	Leu	Ile	Thr	Glu	Asp	Lys	Pro	225	230	235	240
Ile	Arg	Ile	Gly	Leu	Ser	Ala	Thr	Ile	Gly	Ser	Glu	Glu	Lys	Val	Arg	245	250	255	
Leu	Trp	Met	Glu	Ala	Asp	Glu	Val	Val	Lys	Pro	Arg	Leu	Lys	Lys	Lys	260	265	270	
Tyr	Lys	Phe	Thr	Val	Leu	Tyr	Pro	Gln	Pro	Ile	Pro	Glu	Asp	Glu	Lys	275	280	285	
Leu	Ala	Glu	Glu	Leu	Lys	Val	Pro	Ile	Glu	Val	Ala	Thr	Arg	Leu	Arg	290	295	300	
Val	Val	Trp	Asp	Ile	Val	Glu	Lys	His	Lys	Lys	Val	Leu	Ile	Phe	Val	305	310	315	320
Asn	Thr	Arg	Gln	Phe	Ala	Glu	Ile	Leu	Gly	His	Arg	Leu	Lys	Ala	Trp	325	330	335	
Gly	Lys	Pro	Val	Glu	Val	His	His	Gly	Ser	Leu	Ser	Arg	Glu	Ala	Arg	340	345	350	
Ile	Glu	Ala	Glu	Lys	Lys	Leu	Lys	Glu	Gly	Lys	Ile	Lys	Ala	Leu	Ile	355	360	365	
Cys	Thr	Ser	Ser	Met	Glu	Leu	Gly	Ile	Asp	Ile	Gly	Asp	Val	Asp	Ala	370	375	380	
Val	Ile	Gln	Tyr	Met	Ser	Pro	Arg	Gln	Val	Asn	Arg	Leu	Val	Gln	Arg	385	390	395	400
Ala	Gly	Arg	Ser	Lys	His	Arg	Leu	Trp	Glu	Thr	Ser	Glu	Ala	Tyr	Ile	405	410	415	
Ile	Thr	Thr	Asn	Val	Glu	Asp	Tyr	Leu	Gln	Ser	Leu	Ala	Ile	Ala	Lys	420	425	430	
Leu	Ala	Leu	Glu	Gly	Lys	Leu	Glu	Asp	Val	Asn	Pro	Tyr	Glu	Asn	Ala	435	440	445	
Leu	Asp	Val	Leu	Ala	His	Phe	Ile	Val	Gly	Leu	Thr	Ile	Glu	Tyr	Arg	450	455	460	
Asn	Val	Asn	Ile	Thr	Glu	Pro	Tyr	Ser	Leu	Ala	Lys	Ser	Thr	Tyr	Pro	465	470	475	480
Tyr	Arg	Lys	Leu	Ser	Trp	Glu	Asp	Tyr	Gln	Lys	Val	Leu	Glu	Ile	Leu	485	490	495	
Glu	Glu	Ala	Arg	Ile	Ile	Arg	Arg	Asp	Gly	Asp	Ala	Ile	Lys	Leu	Gly	500	505	510	
Lys	Asn	Ala	Phe	Lys	Tyr	Tyr	Phe	Glu	Asn	Leu	Ser	Thr	Ile	Pro	Asp	515	520	525	
Glu	Ile	Ser	Tyr	Ala	Val	Ile	Asp	Ile	Ala	Ser	Gly	Lys	Ser	Val	Gly	530	535	540	
Arg	Leu	Asp	Glu	Asn	Phe	Val	Thr	Glu	Leu	Glu	Glu	Ser	Met	Glu	Phe				

545	550	555	560
Ile Met His Gly Arg Ser Trp Ile Val Leu Glu Ile Asn Glu Lys Glu	565	570	575
Arg Ile Ile Lys Val Lys Glu Ser Asn Asn Leu Glu Ser Ala Leu Pro	580	585	590
Ser Trp Glu Gly Glu Leu Ile Pro Val Pro Leu Glu Val Ala Glu Phe	595	600	605
Val Gly Lys Leu Lys Arg Glu Leu Leu Trp Asp Lys Glu Arg Ala Leu	610	615	620
Lys Leu Leu Glu Gly Val Glu Phe Asn Lys Glu Glu Leu Glu Val Ala	625	630	635
Ile Ser Gln Leu Val Glu Ser Glu Pro Val Ala Ser Asp Arg Asp Ile	645	650	655
Ile Ile Glu Ser Tyr Pro Lys Phe Val Ile Ile His Ala Asp Phe Gly	660	665	670
Asn Lys Ile Asn Glu Gly Leu Thr Arg Phe Ile Ser Val Phe Leu Ser	675	680	685
Ala Arg Tyr Gly Asn Ile Phe Leu Pro Arg Ser Gln Ala His Gly Ile	690	695	700
Ile Ile Arg Ser Pro Phe Arg Leu Asn Pro Glu Glu Ile Lys Glu Ile	705	710	715
Leu Leu Met Lys Ala Glu Val Gly Asp Ile Val Ala Arg Gly Ile Arg	725	730	735
Asp Thr Pro Ile Tyr Arg Trp Lys Met Ser Ala Ile Ala Lys Arg Phe	740	745	750
Gly Ala Leu Arg Arg Asp Ala Arg Ile Lys Lys Val Glu Arg Leu Phe	755	760	765
Glu Gly Thr Ile Ile Glu Lys Glu Thr Phe Asn Glu Ile Tyr His Asp	770	775	780
Lys Ile Asp Ile Asp Lys Thr Glu Lys Ile Leu Glu Lys Ile Arg Lys	785	790	795
Gly Glu Ile Arg Met Lys Thr Leu Phe Arg Glu Glu Ile Thr Pro Leu	805	810	815
Ser Ser Ser Leu Ala Thr Leu Gly Gly Glu Phe Leu Ile Arg Asp Ile	820	825	830
Leu Thr Gln Glu Glu Val Glu Glu Ile Phe Arg Glu Lys Leu Leu Asp	835	840	845
Ala Glu Leu Val Met Val Cys Thr Asn Cys Gly Phe Ser Trp Arg Thr	850	855	860
Lys Val Arg Arg Val Met Asp Arg Val Asn Glu Leu Ser Cys Pro Lys	865	870	875
			880

Cys Asp Ser Lys Met Ile Ala Pro Leu His Pro Lys Asp Ser Glu Thr  
 885 890 895  
 Phe Ile Ser Ala Leu Lys Lys Leu Lys Arg Gly Glu Lys Leu Ser Arg  
 900 905 910  
 Glu Glu Glu Lys Tyr Tyr Leu Arg Gly Leu Lys Ala Ala Asp Leu Leu  
 915 920 925  
 Lys Ala Tyr Gly Lys Asp Ala Leu Leu Ala Leu Ala Thr Tyr Gly Val  
 930 935 940  
 Gly Val Glu Ser Ala Thr Arg Ile Leu Arg Asp Tyr Arg Gly Lys Ser  
 945 950 955 960  
 Leu Ile Lys Ala Leu Ile Glu Ala Glu Lys His Tyr Ile Gln Thr Arg  
 965 970 975  
 Lys Phe Trp Glu  
 980

<210> 77  
 <211> 764  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Helicase 5

<400> 77  
 Val Met Leu Leu Arg Arg Asp Leu Ile Gln Pro Arg Ile Tyr Gln Glu  
 1 5 10 15  
 Val Ile Tyr Ala Lys Cys Lys Glu Thr Asn Cys Leu Ile Val Leu Pro  
 20 25 30  
 Thr Gly Leu Gly Lys Thr Leu Ile Ala Met Met Ile Ala Glu Tyr Arg  
 35 40 45  
 Leu Thr Lys Tyr Gly Gly Lys Val Leu Met Leu Ala Pro Thr Lys Pro  
 50 55 60  
 Leu Val Leu Gln His Ala Glu Ser Phe Arg Arg Leu Phe Asn Leu Pro  
 65 70 75 80  
 Pro Glu Lys Ile Val Ala Leu Thr Gly Glu Lys Ser Pro Glu Glu Arg  
 85 90 95  
 Ser Lys Ala Trp Ala Arg Ala Lys Val Ile Val Ala Thr Pro Gln Thr  
 100 105 110  
 Ile Glu Asn Asp Leu Leu Ala Gly Arg Ile Ser Leu Glu Asp Val Ser  
 115 120 125  
 Leu Ile Val Phe Asp Glu Ala His Arg Ala Val Gly Asn Tyr Ala Tyr  
 130 135 140  
 Val Phe Ile Ala Arg Glu Tyr Lys Arg Gln Ala Lys Asn Pro Leu Val  
 145 150 155 160

Ile Gly Leu Thr Ala Ser Pro Gly Ser Thr Pro Glu Lys Ile Met Glu  
 165 170 175  
 Val Ile Asn Asn Leu Gly Ile Glu His Ile Glu Tyr Arg Ser Glu Asn  
 180 185 190  
 Ser Pro Asp Val Arg Pro Tyr Val Lys Gly Ile Arg Phe Glu Trp Val  
 195 200 205  
 Arg Val Asp Leu Pro Glu Ile Tyr Lys Glu Val Arg Lys Leu Leu Arg  
 210 215 220  
 Glu Met Leu Arg Asp Ala Leu Lys Pro Leu Ala Glu Thr Gly Leu Leu  
 225 230 235 240  
 Glu Ser Ser Ser Pro Asp Ile Pro Lys Lys Glu Val Leu Arg Ala Gly  
 245 250 255  
 Gln Ile Ile Asn Glu Glu Met Ala Lys Gly Asn His Asp Leu Arg Gly  
 260 265 270  
 Leu Leu Leu Tyr His Ala Met Ala Leu Lys Leu His His Ala Ile Glu  
 275 280 285  
 Leu Leu Glu Thr Gln Gly Leu Ser Ala Leu Arg Ala Tyr Ile Lys Lys  
 290 295 300  
 Leu Tyr Glu Glu Ala Lys Ala Gly Ser Thr Lys Ala Ser Lys Glu Ile  
 305 310 315 320  
 Phe Ser Asp Lys Arg Met Lys Lys Ala Ile Ser Leu Leu Val Gln Ala  
 325 330 335  
 Lys Glu Ile Gly Leu Asp His Pro Lys Met Asp Lys Leu Lys Glu Ile  
 340 345 350  
 Ile Arg Glu Gln Leu Gln Arg Lys Gln Asn Ser Lys Ile Ile Val Phe  
 355 360 365  
 Thr Asn Tyr Arg Glu Thr Ala Lys Lys Ile Val Asn Glu Leu Val Lys  
 370 375 380  
 Asp Gly Ile Lys Ala Lys Arg Phe Val Gly Gln Ala Ser Lys Glu Asn  
 385 390 395 400  
 Asp Arg Gly Leu Ser Gln Arg Glu Gln Lys Leu Ile Leu Asp Glu Phe  
 405 410 415  
 Ala Arg Gly Glu Phe Asn Val Leu Val Ala Thr Ser Val Gly Glu Glu  
 420 425 430  
 Gly Leu Asp Val Pro Glu Val Asp Leu Val Val Phe Tyr Glu Pro Val  
 435 440 445  
 Pro Ser Ala Ile Arg Ser Ile Gln Arg Arg Gly Arg Thr Gly Arg His  
 450 455 460  
 Met Pro Gly Arg Val Ile Ile Leu Met Ala Lys Gly Thr Arg Asp Glu  
 465 470 475 480

Ala	Tyr	Tyr	Trp	Ser	Ser	Arg	Gln	Lys	Glu	Lys	Ile	Met	Gln	Glu	Thr		
				485					490					495			
Ile	Ala	Lys	Val	Ser	Gln	Ala	Ile	Lys	Lys	Gln	Lys	Gln	Thr	Ser	Leu		
			500					505					510				
Val	Asp	Phe	Val	Arg	Glu	Lys	Glu	Ser	Glu	Lys	Thr	Ser	Leu	Asp	Lys		
		515					520					525					
Trp	Leu	Lys	Lys	Glu	Lys	Glu	Glu	Ala	Thr	Glu	Lys	Glu	Glu	Lys	Lys		
	530					535						540					
Val	Lys	Ala	Gln	Glu	Gly	Val	Lys	Val	Val	Val	Asp	Ser	Arg	Glu	Leu		
545					550					555					560		
Arg	Ser	Glu	Val	Val	Lys	Arg	Leu	Lys	Leu	Leu	Gly	Val	Lys	Leu	Glu		
				565					570					575			
Val	Lys	Thr	Leu	Asp	Val	Gly	Asp	Tyr	Ile	Ile	Ser	Glu	Asp	Val	Ala		
			580					585					590				
Ile	Glu	Arg	Lys	Ser	Ala	Asn	Asp	Phe	Ile	Gln	Ser	Ile	Ile	Asp	Gly		
		595					600					605					
Arg	Leu	Phe	Asp	Gln	Val	Lys	Arg	Leu	Lys	Glu	Ala	Tyr	Ser	Arg	Pro		
	610					615						620					
Ile	Met	Ile	Val	Glu	Gly	Ser	Leu	Tyr	Gly	Ile	Arg	Asn	Val	His	Pro		
625					630					635					640		
Asn	Ala	Ile	Arg	Gly	Ala	Ile	Ala	Ala	Val	Thr	Val	Asp	Phe	Gly	Val		
				645					650					655			
Pro	Ile	Ile	Phe	Ser	Ser	Thr	Pro	Glu	Glu	Thr	Ala	Gln	Tyr	Ile	Phe		
			660					665					670				
Leu	Ile	Ala	Lys	Arg	Glu	Gln	Glu	Glu	Arg	Glu	Lys	Pro	Val	Arg	Ile		
	675					680						685					
Arg	Ser	Glu	Lys	Lys	Ala	Leu	Thr	Leu	Ala	Glu	Arg	Gln	Arg	Leu	Ile		
	690					695						700					
Val	Glu	Gly	Leu	Pro	His	Val	Ser	Ala	Thr	Leu	Ala	Arg	Arg	Leu	Leu		
705					710					715					720		
Lys	His	Phe	Gly	Ser	Val	Glu	Arg	Val	Phe	Thr	Ala	Ser	Val	Ala	Glu		
				725					730					735			
Leu	Met	Lys	Val	Glu	Gly	Ile	Gly	Glu	Lys	Ile	Ala	Lys	Glu	Ile	Arg		
		740						745					750				
Arg	Val	Ile	Thr	Ala	Pro	Tyr	Ile	Glu	Asp	Glu	Glu						
		755					760										

<210> 78

<211> 940

<212> PRT

<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Helicase 6

<400> 78

Leu	Lys	Gly	Leu	Phe	Arg	Asp	Val	Ile	Leu	His	Asn	Pro	His	Leu	Phe	1	5	10	15
Val	Tyr	Ser	Tyr	Ser	Asp	Lys	Gly	Ile	Ile	Pro	Phe	Lys	His	Gln	Phe	20	25	30	
Gln	Thr	Leu	Tyr	His	Ala	Met	Leu	Met	Arg	Pro	Val	Arg	Leu	Met	Ile	35	40	45	
Ala	Asp	Glu	Ile	Gly	Leu	Gly	Lys	Thr	Ile	Gln	Ala	Leu	Leu	Ile	Ala	50	55	60	
Lys	Tyr	Leu	Asp	Phe	Arg	Gly	Glu	Ile	Glu	Lys	Ala	Leu	Ile	Val	Val	65	70	75	80
Pro	Lys	Val	Leu	Arg	Glu	Gln	Trp	Arg	Glu	Glu	Val	Lys	Arg	Ile	Leu	85	90	95	
Glu	Glu	Ala	Pro	Glu	Val	Ile	Glu	Asn	Gly	Ser	Glu	Ile	Glu	Trp	Lys	100	105	110	
Leu	Lys	Arg	Pro	Arg	Lys	Tyr	Phe	Ile	Ile	Ser	Ile	Asp	Leu	Ala	Lys	115	120	125	
Arg	Tyr	Thr	Glu	Glu	Ile	Leu	Arg	Gln	Lys	Trp	Asp	Leu	Val	Ile	Val	130	135	140	
Asp	Glu	Val	His	Asn	Ala	Thr	Leu	Gly	Thr	Gln	Arg	Tyr	Glu	Phe	Leu	145	150	155	160
Lys	Glu	Leu	Thr	Lys	Asn	Lys	Asp	Leu	Asn	Val	Ile	Phe	Leu	Ser	Ala	165	170	175	
Thr	Pro	His	Arg	Gly	Asn	Asn	Arg	Asp	Tyr	Leu	Ala	Arg	Leu	Arg	Leu	180	185	190	
Leu	Asp	Pro	Thr	Ile	Pro	Glu	Glu	Ile	Ser	Pro	Met	His	Glu	Arg	Lys	195	200	205	
Ile	Tyr	Met	Lys	Ser	Arg	Gly	Thr	Leu	Val	Leu	Arg	Arg	Thr	Lys	Lys	210	215	220	
Val	Val	Asn	Glu	Leu	Glu	Gly	Glu	Val	Phe	Lys	Lys	Cys	His	Phe	Gly	225	230	235	240
Ala	Val	Val	Val	Glu	Val	Ser	Arg	Glu	Glu	Arg	Glu	Phe	Phe	Glu	Glu	245	250	255	
Leu	Asn	Arg	Ala	Leu	Phe	Glu	Leu	Ile	Lys	Asp	Gln	Ala	Asp	Tyr	Ser	260	265	270	
Pro	Leu	Thr	Leu	Leu	Ala	Val	Ile	Ile	Arg	Lys	Arg	Ala	Ser	Ser	Ser	275	280	285	
Tyr	Glu	Ala	Ala	Leu	Lys	Thr	Leu	Thr	Arg	Ile	Val	Glu	Ser	Ala	Tyr	290	295	300	
Ile	Ser	Gly	Gln	Glu	Arg	Ala	Arg	Gly	Val	Glu	Ser	Tyr	Ile	Glu	Lys				

305		310		315		320
Ile Phe Arg Met Gly Tyr Glu Glu Leu Glu Ile Glu Glu Phe Asn Glu	325		330		335	
Ile Asp Asp Ala Ile His Lys Ile Ile Asp Glu Tyr Arg Gly Phe Leu	340		345		350	
Thr Glu Glu Gln Leu Glu Arg Leu Arg Arg Val Leu Glu Leu Gly Lys	355		360		365	
Lys Ile Gly Ser Lys Asp Ser Lys Leu Glu Val Ile Ser Asp Ile Val	370		375		380	
Ala Tyr His Ile Arg Asn Gly Glu Lys Val Ile Ile Phe Thr Glu Phe	385		390		395	400
Arg Asp Thr Leu Glu Tyr Val Leu Glu Arg Leu Pro Asp Ile Leu Arg	405		410		415	
Arg Lys His Gly Ile Val Leu Glu Lys Asp Asp Ile Ala Lys Leu His	420		425		430	
Gly Gly Met Lys Ser Glu Glu Ile Glu Arg Glu Ile Asn Lys Phe His	435		440		445	
Glu Arg Ala Asn Leu Leu Val Ser Thr Asp Val Ala Ser Glu Gly Leu	450		455		460	
Asn Leu His Val Ala Ser Val Val Ile Asn Tyr Glu Ala Pro Trp Ser	465		470		475	480
Pro Ile Lys Leu Glu Gln Arg Val Gly Arg Ile Trp Arg Leu Asn Gln	485		490		495	
Thr Arg Glu Thr Lys Ala Tyr Thr Ile Phe Leu Ala Thr Glu Thr Asp	500		505		510	
Leu Asp Val Leu Asn Asn Leu Tyr Arg Lys Ile Met Asn Ile Lys Glu	515		520		525	
Ala Val Gly Ser Gly Pro Ile Ile Gly Arg Pro Ile Phe Glu Gly Asp	530		535		540	
Phe Glu Asn Leu Trp Asn Glu Gly Ala Glu Glu Glu Asn Arg Glu Val	545		550		555	560
Ser Glu Tyr Glu Leu Ile Leu Ala Ser Ile Lys Gly Glu Leu Lys Gly	565		570		575	
Tyr Ala Gly Ala Leu Val Arg Thr Leu Arg Ile Leu Lys Gln Lys Val	580		585		590	
Glu Gly Ala Val Pro Val Asn Pro Ala Gly Ser Ile Arg Arg Glu Leu	595		600		605	
Glu Ile Ile Leu Glu Asp Thr Pro Asp Val Glu Val Leu Lys Lys Ile	610		615		620	
Val Asn Arg Asn Val Pro Asn Pro Phe Arg Leu Val Arg Gly Leu Leu	625		630		635	640

Arg Glu Ala Glu Gly Ile Glu Gly Ile Arg Val Leu Val Lys Gly Tyr  
 645 650 655  
 Asp Gly Ser Met Asp Val Tyr Tyr Ala Ile Phe Tyr Asp Glu Asp Gly  
 660 665 670  
 Arg Glu Ile Tyr Arg Tyr Pro Ile Leu Ala Glu Asn Gly Lys Tyr Leu  
 675 680 685  
 Val Gly Phe Asn Leu Leu Lys Arg Ile Ser Glu Val Leu Ser Lys Glu  
 690 695 700  
 Tyr Lys Val Val Arg Gly Ala Ser Glu Glu Val Asp Tyr Lys Val Lys  
 705 710 715 720  
 Thr Leu Val Met Asp Asn Ile Tyr Asn Leu Ile Val Lys Lys Tyr Leu  
 725 730 735  
 Glu Tyr Asp Ser Leu Asn Ile Lys Glu Gly Lys Ile Phe Lys Arg Leu  
 740 745 750  
 Lys Val Glu Ile Lys Lys Ala Leu Glu Val Lys Gly Ile Ser Glu Glu  
 755 760 765  
 Glu Phe Glu Val Ile Lys Arg Val Pro Pro Glu Ile Met Glu Val Leu  
 770 775 780  
 Gly Leu Asp Ser Thr Lys Ile Glu Leu Pro Thr Asn Glu Tyr Leu Lys  
 785 790 795 800  
 Ile Phe Glu Arg Asn Phe Val Pro Leu Asp Lys Ile Leu Glu Ser Glu  
 805 810 815  
 Lys Lys Ala Met Glu Ile Val Met Glu Leu Glu Lys Ser Arg Gly Tyr  
 820 825 830  
 Asn Val Glu Asp Val Ser Leu Arg Glu His Tyr Asp Ile Arg Ala Phe  
 835 840 845  
 Thr Asp Gly Glu Glu Lys Tyr Ile Glu Val Lys Gly His Tyr Pro Met  
 850 855 860  
 Leu Leu Leu Ala Glu Leu Thr Glu Lys Glu Phe Glu Phe Ala Gln Lys  
 865 870 875 880  
 Asn Glu Asp Lys Tyr Trp Ile Tyr Ile Val Ser Asn Ile Ala Lys Asp  
 885 890 895  
 Pro Val Ile Val Lys Ile Tyr Lys Pro Phe Ser Gln Asp Arg Arg Val  
 900 905 910  
 Phe Val Val Lys Asn Gly Glu Asp Val Glu Val Asn Ile Asn Ile Glu  
 915 920 925  
 Ile Lys Lys Lys Asp Arg His Leu Leu Lys Leu Ser  
 930 935 940

<210> 79  
 <211> 1278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 7

<400> 79

Val	Ile	Thr	Leu	Glu	Leu	His	Pro	Ser	Glu	Ile	Ala	Arg	Tyr	Phe	Glu	
1				5					10					15		
Leu	Glu	Glu	Cys	Ser	His	Tyr	Phe	Ser	Asn	Leu	Leu	Leu	Arg	Lys	Arg	
			20					25					30			
Gly	Glu	Leu	Gln	Glu	Phe	Glu	Pro	Ile	Ile	Arg	Arg	Lys	Glu	Ile	Glu	
		35					40					45				
Thr	Ile	Glu	Leu	Ala	Lys	Trp	Gly	Asp	Glu	Phe	Glu	Leu	Ser	Leu	Leu	
	50					55					60					
Gln	Glu	Phe	Lys	Lys	Gly	Glu	Ala	Leu	Lys	Lys	Leu	Gly	Val	Lys	Glu	
65					70					75					80	
Leu	Pro	Arg	Phe	Tyr	Gly	Phe	Leu	Thr	Glu	Asn	Asp	Thr	Pro	Val	Arg	
				85					90					95		
Lys	Phe	Phe	Glu	Lys	Tyr	Phe	Lys	Asp	Gly	Ile	Ile	Val	Glu	Glu	Asp	
			100					105					110			
Pro	Asp	Lys	Leu	Leu	Glu	Ile	Ile	Asn	Ser	Glu	Lys	Ser	Ala	Val	Ile	
		115					120					125				
Tyr	Gln	Ala	Pro	Leu	Lys	Gly	Arg	Ile	Gly	Lys	Phe	Asp	Val	Ser	Gly	
	130					135					140					
Arg	Ala	Asp	Phe	Ile	Ile	Lys	Val	Gly	Lys	Thr	Leu	Tyr	Leu	Leu	Glu	
145					150					155					160	
Ala	Lys	Phe	Thr	Lys	Glu	Glu	Lys	Phe	Tyr	His	Arg	Ile	Gln	Ala	Ile	
				165					170					175		
Ile	Tyr	Ala	His	Leu	Leu	Ser	Gln	Met	Ile	Glu	Gly	Tyr	Glu	Ile	Lys	
		180						185					190			
Leu	Ala	Val	Val	Thr	Lys	Glu	Asn	Phe	Pro	Ile	Pro	Ser	Asn	Phe	Leu	
		195					200					205				
Arg	Phe	Pro	Gly	Asp	Val	Glu	Glu	Leu	Lys	Ile	Thr	Leu	Glu	Glu	Lys	
	210					215					220					
Leu	Gly	Gly	Ile	Leu	Arg	Glu	Gln	Glu	Leu	Trp	Ile	Asp	Ala	Arg	Cys	
225					230					235					240	
Thr	Thr	Cys	Pro	Phe	Glu	Ala	Leu	Cys	Leu	Ser	Lys	Ala	Leu	Glu	Glu	
				245					250					255		
Arg	Ser	Leu	Gly	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Ile	Ile	Arg	Ile	Leu	
		260						265					270			
Lys	Glu	Glu	Gly	Ile	Lys	Asp	Leu	Lys	Asp	Met	Ala	Lys	Leu	Phe	Glu	
		275					280					285				

Phe Lys Glu Asn Ser Pro Thr Asn Phe Glu Glu Pro Ser Ile Lys Asp  
 290 295 300

Pro Lys Lys Thr Gln Glu Ile Ala Lys Arg Thr Gly Ile Asn Leu Leu  
 305 310 315 320

Lys Leu Ser Arg Ile Ala Gln Ala Ile Leu Lys Tyr Leu Asp Glu Gly  
 325 330 335

Glu Thr Thr Pro Leu Phe Ile Pro Arg Thr Gly Tyr Asn Leu Pro Met  
 340 345 350

Asp Glu Arg Val Gly Asp Val Glu Pro Ser Tyr Tyr Pro Pro Arg Ser  
 355 360 365

Leu Val Lys Val Phe Phe Tyr Val Gln Thr Ser Pro Ile Thr Asp Thr  
 370 375 380

Ile Ile Gly Ile Ser Ala Leu Val Lys Asn Arg Gln Asn Gly Glu Arg  
 385 390 395 400

Ile Ile Val Lys Phe Val Asp Glu Pro Pro Ile Glu Val Ser Asp Ala  
 405 410 415

Gln Glu Lys Glu Arg Met Leu Leu Ile Glu Phe Phe Arg Asp Val Ile  
 420 425 430

Asp Ala Val Lys Ser Leu Ser Pro Thr Asp Lys Val Tyr Leu His Met  
 435 440 445

Tyr Phe Tyr Asn Arg Lys Gln Arg Asp Asp Leu Met Asp Ala Val Lys  
 450 455 460

Arg His Lys Glu Ile Arg Glu Asn Asn Ala Val Met Ala Leu Leu Ser  
 465 470 475 480

Leu Arg Arg Ala Ile Asp Trp Glu Ser Phe Ser Ile Ile Lys Asp Glu  
 485 490 495

Ile Ile Arg Arg His Ala Leu Pro Leu Ser Pro Gly Leu Gly Phe Val  
 500 505 510

Thr Val Ala Thr Gln Phe Gly Tyr Arg Trp Arg Arg Asn Lys Thr Phe  
 515 520 525

Ala Arg Met Leu Glu Val Val Ala Arg Arg Glu Asn Gly Lys Ile Asn  
 530 535 540

Leu Lys Thr Leu Leu Asn Ile Ser Glu Thr Gly Ile Gly Pro Glu Tyr  
 545 550 555 560

Tyr Pro Ile Ile Asp Arg Asp Asn Glu Gly Ile Pro Phe Thr Leu Phe  
 565 570 575

Trp Ser Ala Leu Val Lys Leu Ala Thr Glu Glu Asp Asn Ser Arg Ile  
 580 585 590

Lys Arg Asp Ile Arg Asp Ile Leu Ser Gln Met Val Glu Ala Leu Lys  
 595 600 605

Thr Ile Glu Glu Arg Ile Pro Glu Gln Tyr Lys Asp Ala Phe Val Lys

610	615	620
Lys Glu Gly Ile Pro Lys Glu Asp Leu Glu Asn Phe Asp Ile Lys Lys 625 630 635 640		
Glu Glu Leu Ala Asp Ile Leu Leu Glu Tyr Leu Gln Leu Glu Phe Asp 645 650 655		
Ala Arg Phe Arg Glu Arg Ser Glu Tyr Tyr Arg Leu Pro Leu Ser Ile 660 665 670		
Arg Ala Tyr Ser Glu Glu Ser Ala Leu Ile Lys Ile Glu Asn Ile Glu 675 680 685		
Lys Lys Lys Asn Asp Cys Leu Leu Phe Gly Lys Ile Val Leu Ile Asp 690 695 700		
Glu Asn Gly Arg Ile Lys Glu Tyr Asn Pro Lys Glu Val Leu Ile Asp 705 710 715 720		
Ile Asp Glu Gly Ser Leu Val Val Val Thr Pro Lys Lys Phe Leu Asp 725 730 735		
Lys Leu Arg Arg Asp Pro Val Gln Arg Ile Ser Lys Ser Pro Leu Gly 740 745 750		
Ile Val Glu Ala Ile Asp His Glu Thr Gly Lys Val Val Ile Arg Leu 755 760 765		
Ile Arg Val Ser Pro Gly Arg Phe Thr Leu Lys His Ser Lys Phe Ser 770 775 780		
Cys Lys Asn Gly Leu Leu Thr Ile Thr Tyr Pro Glu Gly Glu Val Lys 785 790 795 800		
Val Thr Pro Gly Glu Ile Val Ile Val Asp Pro Ser Val Asp Asp Ile 805 810 815		
Gly Met Glu Arg Ala Tyr Asn Val Leu Ser Glu Ile Ser Gln Gly Glu 820 825 830		
Leu Lys His Glu Ile Tyr Gln Lys Val Lys Ala Ile Tyr Glu Gly Asn 835 840 845		
Thr Glu Ser Arg Tyr Glu Val Asn Ile Trp Lys Lys Lys His Ile Glu 850 855 860		
Glu Phe Leu Ser Arg Val Lys Lys Ile Asn Glu Glu Gln Lys Lys Phe 865 870 875 880		
Ala Ile Asp Ile Asn Asn Phe Leu Val Thr Leu Gln Glu Pro Pro Gly 885 890 895		
Thr Gly Lys Thr Ser Gly Ala Ile Ala Pro Ala Ile Leu Ala Arg Ala 900 905 910		
Tyr Ser Met Val Lys Asp Lys Lys Asn Gly Leu Phe Val Val Thr Gly 915 920 925		
Val Ser His Arg Ala Val Asn Glu Ala Leu Ile Lys Thr Leu Lys Leu 930 935 940		

Lys Lys Glu Leu Glu Asn Thr Leu Lys Glu Leu Arg Lys Ile Asp Leu  
 945 950 955 960  
 Ile Arg Ala Val Ser Gly Glu Glu Ala Ile Lys Ile Ile Lys Glu Glu  
 965 970 975  
 Leu Glu Arg Glu Ile Lys Asp Asp Val Asp Arg Ile Arg Phe Thr Ala  
 980 985 990  
 Gln Glu Ile Thr His Ser Ser Lys Gln Arg Ser Leu Asp Lys Tyr Phe  
 995 1000 1005  
 Ala Asn Ser Gly Thr Val Arg Ile Val Phe Gly Thr Pro Gln Thr Leu  
 1010 1015 1020  
 Asn Lys Leu Met Lys Asn Thr Lys Glu Val Glu Leu Val Val Ile Asp  
 1025 1030 1035 1040  
 Glu Ala Ser Met Met Asp Leu Pro Met Phe Phe Leu Ser Thr Lys Val  
 1045 1050 1055  
 Cys Lys Gly Gln Val Leu Leu Val Gly Asp His Arg Gln Met Glu Pro  
 1060 1065 1070  
 Ile Gln Val His Glu Trp Gln Leu Glu Asp Arg Lys Thr Phe Glu Glu  
 1075 1080 1085  
 His Tyr Pro Phe Leu Ser Ala Leu Asn Phe Ile Arg Phe Leu Arg Gly  
 1090 1095 1100  
 Glu Leu Asp Glu Arg Glu Leu Lys Lys Phe Lys Arg Ile Leu Gly Arg  
 1105 1110 1115 1120  
 Glu Pro Pro Glu Trp Lys Lys Asp Lys Asn Glu Val Leu Pro Leu Tyr  
 1125 1130 1135  
 Arg Leu Val Arg Thr Tyr Arg Leu Pro Gln Glu Ile Ala Asp Leu Leu  
 1140 1145 1150  
 Ser Asp Ala Ile Tyr Arg Ala Asp Gly Ile Lys Leu Ile Ser Glu Lys  
 1155 1160 1165  
 Lys Lys Arg Arg Lys Ile Ile Ala Arg His Lys Asp Glu Phe Leu Ser  
 1170 1175 1180  
 Ile Val Leu Asp Asp Arg Tyr Pro Phe Val Leu Ile Leu His Asp Glu  
 1185 1190 1195 1200  
 Gly Asn Ser Thr Lys Ile Asn Glu Leu Glu Ala Lys Ile Val Glu Lys  
 1205 1210 1215  
 Ile Ile Lys Arg Val Glu Asn Ile Asp Ile Gly Val Val Val Pro Tyr  
 1220 1225 1230  
 Arg Ala Gln Lys Arg Leu Ile Ala Ser Leu Ile Asp Ser Ala Gln Val  
 1235 1240 1245  
 Asp Thr Val Glu Arg Phe Gln Gly Gly Glu Lys Ser Leu Ile Val Ile  
 1250 1255 1260

Ser Met Thr Ser Ser Asp Pro Arg Ile Pro Gly Lys Gly Phe  
1265 1270 1275

<210> 80

<211> 655

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase dna2

<400> 80

Met Asn Ile Lys Ser Phe Ile Asn Arg Leu Lys Glu Leu Val Glu Ile  
1 5 10 15

Glu Arg Glu Ala Glu Ile Glu Ala Met Arg Leu Glu Met Lys Arg Leu  
20 25 30

Ser Gly Val Glu Arg Glu Arg Leu Gly Arg Ala Ile Leu Ser Leu Asn  
35 40 45

Gly Lys Ile Val Gly Glu Glu Leu Gly Tyr Phe Leu Val Lys Tyr Gly  
50 55 60

Arg Asn Lys Glu Ile Lys Thr Glu Ile Ser Val Gly Asp Leu Val Val  
65 70 75 80

Ile Ser Lys Arg Asp Pro Leu Lys Ser Asp Leu Leu Gly Thr Val Val  
85 90 95

Glu Lys Gly Lys Arg Phe Ile Val Val Ala Leu Glu Pro Val Pro Glu  
100 105 110

Trp Ala Leu Arg Asp Val Arg Ile Asp Leu Tyr Ala Asn Asp Ile Thr  
115 120 125

Phe Lys Arg Trp Ile Glu Asn Leu Asp Arg Val Arg Lys Ala Gly Lys  
130 135 140

Lys Ala Leu Glu Phe Tyr Leu Gly Leu Asp Glu Pro Ser Gln Gly Glu  
145 150 155 160

Glu Val Ser Phe Glu Pro Phe Asp Lys Ser Leu Asn Pro Ser Gln Arg  
165 170 175

Lys Ala Ile Ala Lys Ala Leu Gly Ser Glu Asp Phe Phe Leu Ile His  
180 185 190

Gly Pro Phe Gly Thr Gly Lys Thr Arg Thr Leu Val Glu Leu Ile Arg  
195 200 205

Gln Glu Val Lys Arg Gly Asn Lys Val Leu Ala Thr Ala Glu Ser Asn  
210 215 220

Val Ala Val Asp Asn Leu Val Glu Arg Leu Ala Lys Asp Gly Val Lys  
225 230 235 240

Ile Val Arg Val Gly His Pro Ser Arg Val Ser Arg His Leu His Glu  
245 250 255



Thr Thr Leu Ala Tyr Leu Ile Thr Gln His Glu Leu Tyr Gly Glu Leu  
 260 265 270  
 Arg Glu Leu Arg Val Ile Gly Gln Ser Leu Ala Glu Lys Arg Asp Thr  
 275 280 285  
 Tyr Thr Lys Pro Thr Pro Lys Phe Arg Arg Gly Leu Ser Asp Ala Glu  
 290 295 300  
 Ile Ile Lys Leu Ala Glu Lys Gly Arg Gly Ala Arg Gly Leu Ser Ala  
 305 310 315 320  
 Arg Leu Ile Lys Glu Met Ala Glu Trp Ile Lys Leu Asn Arg Gln Val  
 325 330 335  
 Gln Lys Ala Phe Glu Asp Ala Arg Lys Leu Glu Glu Arg Ile Ala Arg  
 340 345 350  
 Asp Ile Ile Arg Glu Ala Asp Val Val Leu Thr Thr Asn Ser Ser Ala  
 355 360 365  
 Ala Leu Asp Val Val Asp Ala Thr Asp Tyr Asp Val Ala Ile Ile Asp  
 370 375 380  
 Glu Ala Thr Gln Ala Thr Ile Pro Ser Ile Leu Ile Pro Leu Asn Lys  
 385 390 395 400  
 Val Asp Arg Phe Ile Leu Ala Gly Asp His Lys Gln Leu Pro Pro Thr  
 405 410 415  
 Ile Leu Ser Leu Glu Ala Gln Glu Leu Ser His Thr Leu Phe Glu Gly  
 420 425 430  
 Leu Ile Glu Lys Tyr Pro Trp Lys Ser Glu Met Leu Thr Ile Gln Tyr  
 435 440 445  
 Arg Met Asn Glu Arg Ile Met Glu Phe Pro Ser Arg Glu Phe Tyr Asp  
 450 455 460  
 Gly Arg Ile Val Ala Asp Glu Ser Val Lys Asn Ile Thr Leu Ala Asp  
 465 470 475 480  
 Leu Gly Ile Lys Val Asn Ala Ser Gly Ile Trp Arg Asp Ile Leu Asp  
 485 490 495  
 Pro Asn Asn Val Leu Val Phe Ile Asp Thr Cys Met Leu Glu Asn Arg  
 500 505 510  
 Phe Glu Arg Gln Arg Arg Gly Ser Glu Ser Arg Glu Asn Pro Leu Glu  
 515 520 525  
 Ala Lys Ile Val Ser Lys Ile Val Glu Lys Leu Leu Glu Ser Gly Val  
 530 535 540  
 Lys Ala Glu Met Met Gly Val Ile Thr Pro Tyr Asp Asp Gln Arg Asp  
 545 550 555 560  
 Leu Ile Ser Leu Asn Val Pro Glu Glu Val Glu Val Lys Thr Val Asp  
 565 570 575  
 Gly Tyr Gln Gly Arg Glu Lys Glu Val Ile Ile Leu Ser Phe Val Arg

580

585

590

Ser Asn Lys Ala Gly Glu Ile Gly Phe Leu Lys Asp Leu Arg Arg Leu  
 595 600 605

Asn Val Ser Leu Thr Arg Ala Lys Arg Lys Leu Ile Met Ile Gly Asp  
 610 615 620

Ser Ser Thr Leu Ser Ser His Glu Thr Tyr Arg Arg Leu Ile Glu His  
 625 630 635 640

Val Arg Glu Lys Gly Leu Tyr Val Val Leu Thr Lys Asp Ser Ile  
 645 650 655

&lt;210&gt; 81

&lt;211&gt; 2163

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Recombinant  
 helicase 8

&lt;400&gt; 81

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atgagggttg atgagctgag agttgatgag aggataaaga gtactttgaa ggagagaggt 60
atcgaatcct tttaccctcc ccaagccgag gccttaaaga gcgggatatt ggaaggtaag 120
aatgcattaa tttcaattcc aacggccagc ggaaaaacac taattgctga gattgccatg 180
gttcatagga ttttgaccca gggaggaaag gctgtataca tagtcccgtc gaaggccttg 240
gctgaagaaa agtttcagga gttccaggat tgggagaaga ttgggttaag agtagcgatg 300
gccactgggg attacgactc aaaggatgag tggttgggga aatacgacat aatcattgcg 360
acggctgaga agtttgattc ccttttaagg catggctcaa gttggattaa ggatgtgaag 420
attttagttg ctgacgagat tcatttgatt ggttcaagag acagaggagc tacgcttgaa 480
gttatcctag ctcatatgct cggaaaggcc caaataattg gactctctgc aacgatagga 540
aatccagagg agcttgcgga gtggttaaat gccgagctaa tagtcagtga ctggaggccc 600
gttaagctta gaaggggagt tttttacca ggcctttgta cctgggaaga tgggaagtata 660
gacaggtttt cctcctggga agagttagtt tacgatgcaa ttaggaagaa gaaaggagcg 720
ctaatttttg taaacatgag aaggaaggct gagagagtag ctttgagct ttctaaaaaa 780
gttaagtctc tcctcacgaa acctgagatt agagctttaa atgaattggc tgattccctc 840
gaggaaaatc ccacaaatga aaagctagct aaggccatta ggggtggagt tgcgttcac 900
cacgctggtc ttgggagaga tgagaggggt ctcgtggagg agaactttag aaagggtata 960
ataaaggccg tagttgccac cccaacactt tcggcgggaa ttaacactcc agcgtttagg 1020
gtgattataa gggatatttg gaggtactct gactttggaa tggagagaat tccgataatc 1080
gaggttcacc aaatgcttgg gagagctgga aggccgaagt atgatgaggt tggggaggga 1140
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cctgaaaaac tgttctccca gctctccaac gagagtaatt tgagaagtca agttttggcc 1260
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ttctatgctt atcaaaggaa ggacacatac tctttagagg agaagataag gaacatactc 1380
tacttcctcc tagagaatga gttcatagag atatccttag aggataaaat aaggccgctt 1440
tccttgggaa ttaggactgc aaagctttat atcgatccct atacggccaa gatgttcaag 1500
gataaaatgg aggaagtgtg taaagatcca aatcctatag gaatatttca cttaatctcc 1560
ctaactccgg atataacccc cttcaactac tcaaagagag aatttgaaag gctcgaagag 1620
gaatactacg aattcaagga taggttatac tttgacgac cctacatttc gggttacgac 1680
ccctacctag agaggaagtt cttcagagct ttcaaaaactg cactagtgtc tctggcatgg 1740
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tataggatag ttgagacggc tgagtggctg gtgtactctc taaaggaaat tgcaaaagtt 1860
cttgagactt atgagatcgt tgattatctt gaaacattga gggttagggt caagtatggg 1920
attagggagg aattgattcc cctaatagca ctcccgttg ttggaagaag gagagctaga 1980
gctctttaca atagcggatt tagaagtata gaggatatat ctcaagcgag gccagaagag 2040
cttttgaaaa tcgaggggat aggggtcaag accgttgagg ctatcttcaa gtttcttgg 2100
aagaatgtga aaatttcgga gaaacctaga aaaagtaccc ttgattactt tctcaaactc 2160

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2163

<213> Artificial Sequence

<223> Description of Artificial Sequence: Recombinant helicase 8

Met Arg Val Asp Glu Leu Arg Val Asp Glu Arg Ile Lys Ser Thr Leu  
1 5 10 15

Lys Glu Arg Gly Ile Glu Ser Phe Tyr Pro Pro Gln Ala Glu Ala Leu  
20 25 30

Lys Ser Gly Ile Leu Glu Gly Lys Asn Ala Leu Ile Ser Ile Pro Thr  
35 40 45

Ala Ser Gly Lys Thr Leu Ile Ala Glu Ile Ala Met Val His Arg Ile  
50 55 60

Leu Thr Gln Gly Gly Lys Ala Val Tyr Ile Val Pro Leu Lys Ala Leu  
65 70 75 80

Ala Glu Glu Lys Phe Gln Glu Phe Gln Asp Trp Glu Lys Ile Gly Leu  
85 90 95

Arg Val Ala Met Ala Thr Gly Asp Tyr Asp Ser Lys Asp Glu Trp Leu  
100 105 110

Gly Lys Tyr Asp Ile Ile Ile Ala Thr Ala Glu Lys Phe Asp Ser Leu  
115 120 125

Leu Arg His Gly Ser Ser Trp Ile Lys Asp Val Lys Ile Leu Val Ala  
130 135 140

Asp Glu Ile His Leu Ile Gly Ser Arg Asp Arg Gly Ala Thr Leu Glu  
145 150 155 160

Val Ile Leu Ala His Met Leu Gly Lys Ala Gln Ile Ile Gly Leu Ser  
165 170 175

Ala Thr Ile Gly Asn Pro Glu Glu Leu Ala Glu Trp Leu Asn Ala Glu  
180 185 190

Leu Ile Val Ser Asp Trp Arg Pro Val Lys Leu Arg Arg Gly Val Phe  
195 200 205

Tyr Gln Gly Phe Val Thr Trp Glu Asp Gly Ser Ile Asp Arg Phe Ser  
210 215 220

Ser Trp Glu Glu Leu Val Tyr Asp Ala Ile Arg Lys Lys Lys Gly Ala  
225 230 235 240

Leu Ile Phe Val Asn Met Arg Arg Lys Ala Glu Arg Val Ala Leu Glu.  
245 250 255

Leu Ser Lys Lys Val Lys Ser Leu Leu Thr Lys Pro Glu Ile Arg Ala  
 260 265 270  
 Leu Asn Glu Leu Ala Asp Ser Leu Glu Glu Asn Pro Thr Asn Glu Lys  
 275 280 285  
 Leu Ala Lys Ala Ile Arg Gly Gly Val Ala Phe His His Ala Gly Leu  
 290 295 300  
 Gly Arg Asp Glu Arg Val Leu Val Glu Glu Asn Phe Arg Lys Gly Ile  
 305 310 315 320  
 Ile Lys Ala Val Val Ala Thr Pro Thr Leu Ser Ala Gly Ile Asn Thr  
 325 330 335  
 Pro Ala Phe Arg Val Ile Ile Arg Asp Ile Trp Arg Tyr Ser Asp Phe  
 340 345 350  
 Gly Met Glu Arg Ile Pro Ile Ile Glu Val His Gln Met Leu Gly Arg  
 355 360 365  
 Ala Gly Arg Pro Lys Tyr Asp Glu Val Gly Glu Gly Ile Ile Val Ser  
 370 375 380  
 Thr Ser Asp Asp Pro Arg Glu Val Met Asn His Tyr Ile Phe Gly Lys  
 385 390 395 400  
 Pro Glu Lys Leu Phe Ser Gln Leu Ser Asn Glu Ser Asn Leu Arg Ser  
 405 410 415  
 Gln Val Leu Ala Leu Ile Ala Thr Phe Gly Tyr Ser Thr Val Glu Glu  
 420 425 430  
 Ile Leu Lys Phe Ile Ser Asn Thr Phe Tyr Ala Tyr Gln Arg Lys Asp  
 435 440 445  
 Thr Tyr Ser Leu Glu Glu Lys Ile Arg Asn Ile Leu Tyr Phe Leu Leu  
 450 455 460  
 Glu Asn Glu Phe Ile Glu Ile Ser Leu Glu Asp Lys Ile Arg Pro Leu  
 465 470 475 480  
 Ser Leu Gly Ile Arg Thr Ala Lys Leu Tyr Ile Asp Pro Tyr Thr Ala  
 485 490 495  
 Lys Met Phe Lys Asp Lys Met Glu Glu Val Val Lys Asp Pro Asn Pro  
 500 505 510  
 Ile Gly Ile Phe His Leu Ile Ser Leu Thr Pro Asp Ile Thr Pro Phe  
 515 520 525  
 Asn Tyr Ser Lys Arg Glu Phe Glu Arg Leu Glu Glu Glu Tyr Tyr Glu  
 530 535 540  
 Phe Lys Asp Arg Leu Tyr Phe Asp Asp Pro Tyr Ile Ser Gly Tyr Asp  
 545 550 555 560  
 Pro Tyr Leu Glu Arg Lys Phe Phe Arg Ala Phe Lys Thr Ala Leu Val  
 565 570 575  
 Leu Leu Ala Trp Ile Asn Glu Val Pro Glu Gly Glu Ile Val Glu Lys

580

585

590

Tyr Ser Val Glu Pro Gly Asp Ile Tyr Arg Ile Val Glu Thr Ala Glu  
595 600 605

Trp Leu Val Tyr Ser Leu Lys Glu Ile Ala Lys Val Leu Gly Ala Tyr  
610 615 620

Glu Ile Val Asp Tyr Leu Glu Thr Leu Arg Val Arg Val Lys Tyr Gly  
625 630 635 640

Ile Arg Glu Glu Leu Ile Pro Leu Met Gln Leu Pro Leu Val Gly Arg  
645 650 655

Arg Arg Ala Arg Ala Leu Tyr Asn Ser Gly Phe Arg Ser Ile Glu Asp  
660 665 670

Ile Ser Gln Ala Arg Pro Glu Glu Leu Leu Lys Ile Glu Gly Ile Gly  
675 680 685

Val Lys Thr Val Glu Ala Ile Phe Lys Phe Leu Gly Lys Asn Val Lys  
690 695 700

Ile Ser Glu Lys Pro Arg Lys Ser Thr Leu Asp Tyr Phe Leu Lys Ser  
705 710 715 720

&lt;210&gt; 83

&lt;211&gt; 2163

&lt;212&gt; DNA

<213> *Pyrococcus furiosus*

&lt;400&gt; 83

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atcgaatcct	tttaccctcc	ccaagccgag	gccttaaaga	gcgggatatt	ggaaggtaag	120
aatgcattaa	tttcaattcc	aacggccagc	ggaaaaacac	taattgctga	gattgccatg	180
gttcatagga	ttttgaccca	gggaggaaag	gctgtataca	tagtcccgt	gaaggccttg	240
gctgaagaaa	agtttcagga	gttccaggat	tggggagaaga	ttgggttaag	agtagcgatg	300
gccactgggg	attacgactc	aaaggatgag	tgggttgggga	aatacgacat	aatcattgcg	360
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<212> PRT

<213> *Pyrococcus furiosus*

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